



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/584,289

DATE: 07/10/2006

TIME: 10:30:07

Input Set : A:\L7350-0008.txt

Output Set: N:\CRF4\07102006\J584289.raw

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3 <110> APPLICANT: Locomogene, Inc.
5 <120> TITLE OF INVENTION: A method of inhibiting a cancer
7 <130> FILE REFERENCE: G06-0031
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/584,289
C--> 10 <141> CURRENT FILING DATE: 2006-06-23
12 <150> PRIOR APPLICATION NUMBER: JP2003-428300
13 <151> PRIOR FILING DATE: 2003-12-24
15 <160> NUMBER OF SEQ ID NOS: 19
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3374
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (403)..(2256)
27 <223> OTHER INFORMATION:
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34 gattttcttg ccacagcatc cattctgggt aggctggtga tcttctgagt agtgatagat 180
36 tggttggtgg tgaggtttac aggtgttccc ttctcttact cctggtgttg gctacaatca 240
38 ggtggcgtct agagcagcat gggacagggt ggtaagggga gtcttctcat tatgcagaag 300
40 tgatcaactt aaatctctgt cagatctacc tttatgtagc ccggcagtcg cgcggttga 360
42 gcgggctcgc ggcgctgggt tcctggtctc cgggccaggg ca atg ttc cgc acg 414
43 Met Phe Arg Thr
44 1
46 gca gtg atg atg gcg gcc agc ctg gcg ctg acc ggg gct gtg gtg gct 462
47 Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly Ala Val Val Ala
48 5 10 15 20
50 cac gcc tac tac ctc aaa cac cag ttc tac ccc act gtg gtg tac ctg 510
51 His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr Val Val Tyr Leu
52 25 30 35
54 acc aag tcc agc ccc agc atg gca gtc ctg tac atc cag gcc ttt gtc 558
55 Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile Gln Ala Phe Val
56 40 45 50
58 ctt gtc ttc ctt ctg ggc aag gtg atg ggc aag gtg ttc ttt ggg caa 606
59 Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val Phe Phe Gly Gln
60 55 60 65
62 ctg agg gca gca gag atg gag cac ctt ctg gaa cgt tcc tgg tac gcc 654
63 Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg Ser Trp Tyr Ala
64 70 75 80
66 gtc aca gag act tgt ctg gcc ttc acc gtt ttt cgg gat gac ttc agc 702

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67	Val	Thr	Glu	Thr	Cys	Leu	Ala	Phe	Thr	Val	Phe	Arg	Asp	Asp	Phe	Ser	
68	85					90					95					100	
70	ccc	cgc	ttt	gtt	gca	ctc	ttc	act	ctt	ctt	ctc	ttc	ctc	aaa	tgt	ttc	750
71	Pro	Arg	Phe	Val	Ala	Leu	Phe	Thr	Leu	Leu	Leu	Phe	Leu	Lys	Cys	Phe	
72					105					110					115		
74	cac	tgg	ctg	gct	gag	gac	cgt	gtg	gac	ttt	atg	gaa	cgc	agc	ccc	aac	798
75	His	Trp	Leu	Ala	Glu	Asp	Arg	Val	Asp	Phe	Met	Glu	Arg	Ser	Pro	Asn	
76				120					125					130			
78	atc	tcc	tgg	ctc	ttt	cac	tgc	cgc	att	gtc	tct	ctt	atg	ttc	ctc	ctg	846
79	Ile	Ser	Trp	Leu	Phe	His	Cys	Arg	Ile	Val	Ser	Leu	Met	Phe	Leu	Leu	
80			135					140						145			
82	ggc	atc	ctg	gac	ttc	ctc	ttc	gtc	agc	cac	gcc	tat	cac	agc	atc	ctg	894
83	Gly	Ile	Leu	Asp	Phe	Leu	Phe	Val	Ser	His	Ala	Tyr	His	Ser	Ile	Leu	
84		150					155					160					
86	acc	cgt	ggg	gcc	tct	gtg	cag	ctg	gtg	ttt	ggc	ttt	gag	tat	gcc	atc	942
87	Thr	Arg	Gly	Ala	Ser	Val	Gln	Leu	Val	Phe	Gly	Phe	Glu	Tyr	Ala	Ile	
88	165					170					175					180	
90	ctg	atg	acg	atg	gtg	ctc	acc	atc	ttc	atc	aag	tat	gtg	ctg	cac	tcc	990
91	Leu	Met	Thr	Met	Val	Leu	Thr	Ile	Phe	Ile	Lys	Tyr	Val	Leu	His	Ser	
92				185						190					195		
94	gtg	gac	ctc	cag	agt	gag	aac	ccc	tgg	gac	aac	aag	gct	gtg	tac	atg	1038
95	Val	Asp	Leu	Gln	Ser	Glu	Asn	Pro	Trp	Asp	Asn	Lys	Ala	Val	Tyr	Met	
96			200					205					210				
98	ctc	tac	aca	gag	ctg	ttt	aca	ggc	ttc	atc	aag	gtt	ctg	ctg	tac	atg	1086
99	Leu	Tyr	Thr	Glu	Leu	Phe	Thr	Gly	Phe	Ile	Lys	Val	Leu	Leu	Tyr	Met	
100		215					220					225					
102	gcc	ttc	atg	acc	atc	atg	atc	aag	gtg	cac	acc	ttc	cca	ctc	ttt	gcc	1134
103	Ala	Phe	Met	Thr	Ile	Met	Ile	Lys	Val	His	Thr	Phe	Pro	Leu	Phe	Ala	
104		230					235					240					
106	atc	cgg	ccc	atg	tac	ctg	gcc	atg	aga	cag	ttc	aag	aaa	gct	gtg	aca	1182
107	Ile	Arg	Pro	Met	Tyr	Leu	Ala	Met	Arg	Gln	Phe	Lys	Lys	Ala	Val	Thr	
108	245					250					255					260	
110	gat	gcc	atc	atg	tct	cgc	cga	gcc	atc	cgc	aac	atg	aac	acc	ctg	tat	1230
111	Asp	Ala	Ile	Met	Ser	Arg	Arg	Ala	Ile	Arg	Asn	Met	Asn	Thr	Leu	Tyr	
112				265						270					275		
114	cca	gat	gcc	acc	cca	gag	gag	ctc	cag	gca	atg	gac	aat	gtc	tgc	atc	1278
115	Pro	Asp	Ala	Thr	Pro	Glu	Glu	Leu	Gln	Ala	Met	Asp	Asn	Val	Cys	Ile	
116			280						285				290				
118	atc	tgc	cga	gaa	gag	atg	gtg	act	ggg	gcc	aag	aga	ctg	ccc	tgc	aac	1326
119	Ile	Cys	Arg	Glu	Glu	Met	Val	Thr	Gly	Ala	Lys	Arg	Leu	Pro	Cys	Asn	
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122	cac	att	ttc	cat	acc	agc	tgc	ctg	cgc	tcc	tgg	ttc	cag	cgg	cag	cag	1374
123	His	Ile	Phe	His	Thr	Ser	Cys	Leu	Arg	Ser	Trp	Phe	Gln	Arg	Gln	Gln	
124		310					315					320					
126	acc	tgc	ccc	acc	tgc	cgt	atg	gat	gtc	ctt	cgt	gca	tcg	ctg	cca	gcg	1422
127	Thr	Cys	Pro	Thr	Cys	Arg	Met	Asp	Val	Leu	Arg	Ala	Ser	Leu	Pro	Ala	
128	325					330					335					340	
130	cag	tca	cca	cca	ccc	ccg	gag	cct	gcg	gat	cag	ggg	cca	ccc	cct	gcc	1470
131	Gln	Ser	Pro	Pro	Pro	Pro	Glu	Pro	Ala	Asp	Gln	Gly	Pro	Pro	Pro	Ala	

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135	Pro	His	Pro	Pro	Pro	Leu	Leu	Pro	Gln	Pro	Pro	Asn	Phe	Pro	Gln	Gly	
136				360				365				370					
138	ctc	ctg	cct	cct	ttt	cct	cca	ggc	atg	ttc	cca	ctg	tgg	ccc	ccc	atg	1566
139	Leu	Leu	Pro	Pro	Phe	Pro	Pro	Gly	Met	Phe	Pro	Leu	Trp	Pro	Pro	Met	
140			375					380				385					
142	ggc	ccc	ttt	cca	cct	gtc	ccg	cct	ccc	ccc	agc	tca	gga	gag	gct	gtg	1614
143	Gly	Pro	Phe	Pro	Pro	Val	Pro	Pro	Pro	Pro	Ser	Ser	Gly	Glu	Ala	Val	
144		390					395					400					
146	gct	cct	cca	tcc	acc	agt	gca	gca	gcc	ctt	tct	cgg	ccc	agt	gga	gca	1662
147	Ala	Pro	Pro	Ser	Thr	Ser	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Ser	Gly	Ala	
148	405					410				415						420	
150	gct	aca	acc	aca	gct	gct	ggc	acc	agt	gct	act	gct	gct	tct	gcc	aca	1710
151	Ala	Thr	Thr	Thr	Ala	Ala	Gly	Thr	Ser	Ala	Thr	Ala	Ala	Ser	Ala	Thr	
152				425				430				435					
154	gca	tct	ggc	cca	ggc	tct	ggc	tct	gcc	cca	gag	gct	ggc	cct	gcc	cct	1758
155	Ala	Ser	Gly	Pro	Gly	Ser	Gly	Ser	Ala	Pro	Glu	Ala	Gly	Pro	Ala	Pro	
156			440					445				450					
158	ggt	ttc	ccc	ttc	cct	cct	ccc	tgg	atg	ggt	atg	ccc	ctg	cct	cca	ccc	1806
159	Gly	Phe	Pro	Phe	Pro	Pro	Pro	Trp	Met	Gly	Met	Pro	Leu	Pro	Pro	Pro	
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170	gag	gcc	cgg	ctg	cag	agc	ctg	cgt	aac	atc	cac	aca	ctg	ctg	gac	gcc	1950
171	Glu	Ala	Arg	Leu	Gln	Ser	Leu	Arg	Asn	Ile	His	Thr	Leu	Leu	Asp	Ala	
172				505				510				515					
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175	Ala	Met	Leu	Gln	Ile	Asn	Gln	Tyr	Leu	Thr	Val	Leu	Ala	Ser	Leu	Gly	
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179	Pro	Pro	Arg	Pro	Ala	Thr	Ser	Val	Asn	Ser	Thr	Glu	Gly	Thr	Ala	Thr	
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187	Thr	Thr	Pro	Thr	Pro	Gly	Ala	Ser	Pro	Pro	Ala	Pro	Glu	Met	Glu	Arg	
188	565					570				575						580	
190	cct	cca	gct	cct	gag	tca	gtg	ggc	aca	gag	gag	atg	cct	gag	gat	gga	2190
191	Pro	Pro	Ala	Pro	Glu	Ser	Val	Gly	Thr	Glu	Glu	Met	Pro	Glu	Asp	Gly	
192				585				590				595					
194	gag	ccc	gat	gca	gca	gag	ctc	cgc	cgg	cgc	cgc	ctg	cag	aag	ctg	gag	2238
195	Glu	Pro	Asp	Ala	Ala	Glu	Leu	Arg	Arg	Arg	Arg	Leu	Gln	Lys	Leu	Glu	
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208 tccagccttc ctctccaact cttcagccct gtgttctgct ggggccatga aggcagaagg      2526
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232 tgccaaggag ggaccacagg agctgggacc tgccctgcccc tgctcctttcc ccttggtttt      3246
234 gtgttacaag agttgttgga gacagtttca gatgattatt taatttgtaa atattgtaca      3306
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243 <212> TYPE: PRT
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253      20      25      30
256 Val Val Tyr Leu Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile
257      35      40      45
260 Gln Ala Phe Val Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val
261      50      55      60
264 Phe Phe Gly Gln Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg
265 65      70      75      80
268 Ser Trp Tyr Ala Val Thr Glu Thr Cys Leu Ala Phe Thr Val Phe Arg
269      85      90      95
272 Asp Asp Phe Ser Pro Arg Phe Val Ala Leu Phe Thr Leu Leu Leu Phe
273      100     105     110
276 Leu Lys Cys Phe His Trp Leu Ala Glu Asp Arg Val Asp Phe Met Glu
277      115     120     125
280 Arg Ser Pro Asn Ile Ser Trp Leu Phe His Cys Arg Ile Val Ser Leu
281      130     135     140
284 Met Phe Leu Leu Gly Ile Leu Asp Phe Leu Phe Val Ser His Ala Tyr
285 145     150     155     160
288 His Ser Ile Leu Thr Arg Gly Ala Ser Val Gln Leu Val Phe Gly Phe
289      165     170     175

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296 Val Leu His Ser Val Asp Leu Gln Ser Glu Asn Pro Trp Asp Asn Lys
297      195      200      205
300 Ala Val Tyr Met Leu Tyr Thr Glu Leu Phe Thr Gly Phe Ile Lys Val
301      210      215      220
304 Leu Leu Tyr Met Ala Phe Met Thr Ile Met Ile Lys Val His Thr Phe
305 225      230      235      240
308 Pro Leu Phe Ala Ile Arg Pro Met Tyr Leu Ala Met Arg Gln Phe Lys
309      245      250      255
312 Lys Ala Val Thr Asp Ala Ile Met Ser Arg Arg Ala Ile Arg Asn Met
313      260      265      270
316 Asn Thr Leu Tyr Pro Asp Ala Thr Pro Glu Glu Leu Gln Ala Met Asp
317      275      280      285
320 Asn Val Cys Ile Ile Cys Arg Glu Glu Met Val Thr Gly Ala Lys Arg
321      290      295      300
324 Leu Pro Cys Asn His Ile Phe His Thr Ser Cys Leu Arg Ser Trp Phe
325 305      310      315      320
328 Gln Arg Gln Gln Thr Cys Pro Thr Cys Arg Met Asp Val Leu Arg Ala
329      325      330      335
332 Ser Leu Pro Ala Gln Ser Pro Pro Pro Pro Glu Pro Ala Asp Gln Gly
333      340      345      350
336 Pro Pro Pro Ala Pro His Pro Pro Pro Pro Leu Leu Pro Gln Pro Pro Asn
337      355      360      365
340 Phe Pro Gln Gly Leu Leu Pro Pro Phe Pro Pro Gly Met Phe Pro Leu
341      370      375      380
344 Trp Pro Pro Met Gly Pro Phe Pro Pro Val Pro Pro Pro Pro Ser Ser
345 385      390      395      400
348 Gly Glu Ala Val Ala Pro Pro Ser Thr Ser Ala Ala Ala Leu Ser Arg
349      405      410      415
352 Pro Ser Gly Ala Ala Thr Thr Thr Ala Ala Gly Thr Ser Ala Thr Ala
353      420      425      430
356 Ala Ser Ala Thr Ala Ser Gly Pro Gly Ser Gly Ser Ala Pro Glu Ala
357      435      440      445
360 Gly Pro Ala Pro Gly Phe Pro Phe Pro Pro Pro Trp Met Gly Met Pro
361      450      455      460
364 Leu Pro Pro Pro Phe Ala Phe Pro Pro Met Pro Val Pro Pro Ala Gly
365 465      470      475      480
368 Phe Ala Gly Leu Thr Pro Glu Glu Leu Arg Ala Leu Glu Gly His Glu
369      485      490      495
372 Arg Gln His Leu Glu Ala Arg Leu Gln Ser Leu Arg Asn Ile His Thr
373      500      505      510
376 Leu Leu Asp Ala Ala Met Leu Gln Ile Asn Gln Tyr Leu Thr Val Leu
377      515      520      525
380 Ala Ser Leu Gly Pro Pro Arg Pro Ala Thr Ser Val Asn Ser Thr Glu
381      530      535      540
384 Gly Thr Ala Thr Thr Val Val Ala Ala Ala Ser Thr Ser Ile Pro
385 545      550      555      560
388 Ser Ser Glu Ala Thr Thr Pro Thr Pro Gly Ala Ser Pro Pro Ala Pro

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VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27